



App No.:
Titl
Invenors:

09/693,205 Identification of ARSACS . . Thomas J. Hudson, *et al*.



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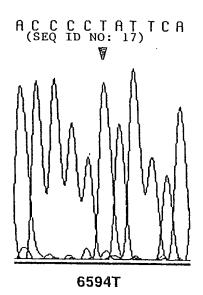
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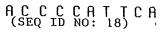
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APPROVED O.G. FIG.

BY CLASS SUBCLASS

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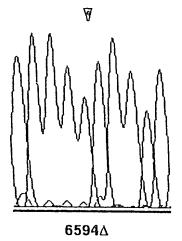


Figure 2A



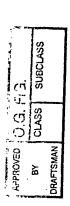
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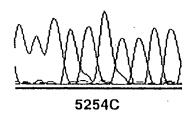
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A A A G C G A C A C (SEQ ID NO: 19)



AAAGHGACAC (SEQ ID NO: 20)

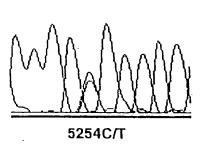


Figure 2B



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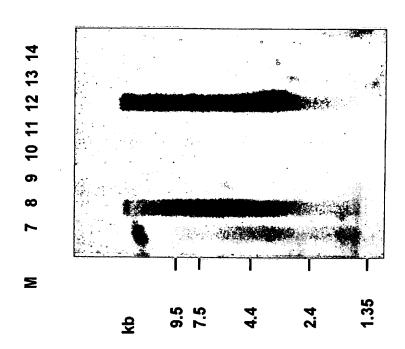
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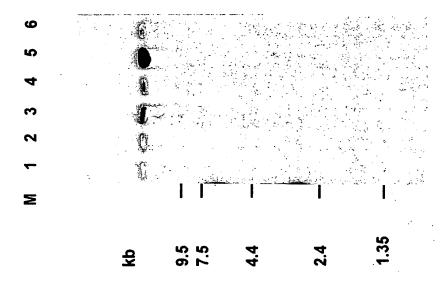


Figure 3

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09/693,205
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exxx Arabidopsis ORF homologous region , dnaJ region highest self homology region heat shock protein homology leucine zipper motifs coiled-coil domains hydrophillic region 3349 3574 rep. 3 2755 2430 2118 TEXTERNAL PROPERTY OF THE PROP 1773 rep. 2 1121 Arabidopsis genornic ORF minimation пиратилизация 500 а.а. 689 rep. 1

Figure 4A



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O.G. FIG. CLASS

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| FLIDWRRNWDIRENLIDPG FLIDWRRNWDIRENLIDPG FY.D.Rd.i.D FLID.,hd.LL.P. | LKRGE-VDKVGK <u>FGL</u> GFNS LKRGE-VDKVGK <u>FGL</u> GFNS .K.GK.G. <u>VG</u> LGFNS .K1Gr <u>PGL</u> GFN. LGV1G. <u>PGV</u> GF.S | Underline = conserved Bold = identical |
|---|---|---|
| GQREPLTVRIKNILEEYPSVSDIFKEILQNADOAN-ATECSFLIDMRRNMDIRENLLDPG GQREPLTVRIKNILEEYPSVSDIFKEILQNADOAN-ATECSFMIDMRRNMDIRENLLDPG GQKE.LT.RIK.ILYPSem.KEILQNADOAATEFV.D.Rd.i.D GQHE.LT.RIK.ILE.YIEIVQNAeOAASE.tFLIDhd.il.P | MAACHGPALWSFINNSQ-F <u>S</u> DS <u>D</u> FVNITRLGESLKRGE-VDKVGK <u>F</u> G <u>L</u> GFNS MAACHGPALWSFINNSe-F <u>S</u> DS <u>D</u> FINITRLGESLKRGE-VDKVGK <u>F</u> G <u>L</u> GFNS .AGPALy <u>N</u> NF <u>L</u> E. <u>D</u> I.LGK.GK.GK.GX_2G <u>L</u> GFNS MAGPALy.F <u>N</u> NSF <u>L</u> DISRIGqa.KiGr <u>P</u> G <u>L</u> GFNL <u>G</u> <u>L</u> <u>E</u> DIRRIGEaLGV.iG· <u>F</u> G <u>L</u> GFN. | VYHITDIPIIMSREFMIMF <u>D</u> P |

705 705 1773 987 18

HSP90 (YEAST)

ARABIDOPSIS

HUMAN-REP 2

MOUSE-REP 1

Figure 4B

 $\dots E.ivMF\overline{D}P$

VYHITD.P. is..... <u>VY</u>HITDIPII<u>M</u>SR-----<u>VY</u>HITDIPII<u>M</u>SR.....

813 813 1879 1093

1830 1044 78

HSP90 (YEAST)

HUMAN-REP 2 ARABIDOPSIS

HUMAN-REP 1 HUMAN-REP 1 HUMAN-REP 1 MOUSE-REP 1

764 764

 $\frac{V\underline{Y}}{I\underline{f}}$.v.D..v \underline{i} Sk...

HSP90 (YEAST)

ARABIDOPSIS

MOUSE-REP 2

09/693,205

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APPROVED O.G. FIG.

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| MNTFWPGRELIVQWYPFDENRNHPSVSWLKMVWKNLYIHFSEDLTLFDEMPLIPRTILEEVs.DKRLL.N. | 60 |
|--|---|
| GQTCVELIRLRIPSLVILDDESEAQLPEFLADIVQKLGGFVLKKLDASIQHPLIKKYIHS DVVTVIRTVV | 120 |
| PLPSAVLQIMEKMPLQKLCNQITSLLPTHKDALRKFLASLTDSSEKEKRIIQELAIFKRIIATT | 180 |
| NHSSDQGISSYTKLKGCKVLHHTAKLPADLRLSISVIDSSDEATIRLANMLKIEQLKTTSDTVKK | 240 |
| CLKLVLKDIENAFYSHEEVTQLMLWVLENLSSLKNENPNVLEWLTPLKFIQISQEQMVSAFGTQISDMHMGHV.A. | 300 |
| GELFDPDIEVLKDLFCNEEGTYFPPSVFTSPDILHSLRQIGLKNEASLKEKDVVQVAKKI.DRYEACTISR | 360 |
| EALQVGACPDQDVLLKKAKTLLLVLNKNHTLLQSSEGKMTLKKIKWVPACKERPPNYPGSSS.QNMQAA | 420 |
| LVWKGDLCNLCAPPDMCDVGHAILIGSSLPLVESIHVNLEKALGIFTKPSLSAVLKHFKIAAV.VVQSTINT | 480 |
| VVDWYSSKTFSDEDYYQFQHILLEIYGFMHDHLNEGKDSFRALKFPWVWTGKKFCPLAQATNN | 540 |
| VIKPIHDLDLQPYLHNVPKTMAKFHQLFKVCGSIEELTSDHISMVIQKIYLKSDQDLSEQTYYAVVEE | 600 |
| ESKQNLHLMLNIIRWLYSNQIPASPNTPVPIHHSKNPSKLIMKPIHECCYCDIKVDDLND | 660 |
| LLEDSVEPIILVHEDIPMKTAEWLKVPCLSTRLINPENMGFEQSGQREPLTVRIKNILEE | 720 |
| | |
| YPSVSDIFKELLQNADDANATECSFLIDMRRNMDIRENLLDPGMAACHGPALWSFNNSQF | 780 |
| YPSVSDIFKELLQNADDANATECSFLIDMRRNMDIRENLLDPGMAACHGPALWSFNNSQF | 780 840 |
| YPSVSDIFKELLQNADDANATECSFLIDMRRNMDIRENLLDPGMAACHGPALWSFNNSQF | |
| YPSVSDIFKELLQNADDANATECSFLIDMRRNMDIRENLLDPGMAACHGPALWSFNNSQF | 840 |
| YPSVSDIFKELLQNADDANATECSFLIDMRRNMDIRENLLDPGMAACHGPALWSFNNSQF | 900 |
| YPSVSDIFKELLQNADDANATECSFLIDMRRNMDIRENLLDPGMAACHGPALWSFNNSQF | 900 960 |
| YPSVSDIFKELLQNADDANATECSFLIDMRRNMDIRENLLDPGMAACHGPALWSFNNSQF | 840 900 960 1020 |
| YPSVSDIFKELLQNADDANATECSFLIDMRRNMDIRENLLDPGMAACHGPALWSFNNSQF | 840 900 960 1020 1080 |
| YPSVSDIFKELLQNADDANATECSFLIDMRRNMDIRENLLDPGMAACHGPALWSFNNSQF | 840 900 960 1020 1080 |
| YPSVSDIFKELLQNADDANATECSFLIDMRRNMDIRENLLDPGMAACHGPALWSFNNSQF | 840 900 960 1020 1080 1140 1200 |
| YPSVSDIFKELLQNADDANATECSFLIDMRRNMDIRENLLDPGMAACHGPALWSFNNSQF | 840 900 960 1020 1080 1140 1200 1260 |

2100

2880

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| IDEKLKIRDPRAKDFAAKYQTIRFLPFLTKPAGFSLDWKGNSFKPETMFAATDLYTAEH |
|---|
| DIVCLLQPILNENSHSFRGCGSVSLAVKEFLGLLKKPTVDLVINQLKEVAKSVDDGITL |

| Q | |
|---|------|
| YQENITNACYKYLHEALMQNEITKMSIIDKLKPFSFILVENAYVDSEKVSFHLNFEAAPYVLMA.ATECVE | 1620 |
| LYQLPNKYKNNFRELFETVGVRQSCTVEDFALVLESIDQERGTKQITEENFQLCRRIISE | 1680 |

| K | |
|--|------|
| GIWSLIREKKQEFCEKNYGKILLPDTNLMLLPAKSLCYNDCPWIKVKDTTVKYCHADIPR | 1740 |

| EVAVKLGAVPKRHKALERYASNVCF TTLGTEFGQKEKLTSRIKSILNAYPSEKEMLKELL | 1800 |
|---|------|
| ONA DDA YA TET CEVED DDOUDYDD I PDDYWA DI OGDA I CVVNNODETEDDVDGI ONI CKC | 1860 |

| | • | | |
|---------------------------|---|-------------------|------|
| TKEGNPYKTGQYGIGFNSVYHITDC | PSFISGNDILCIFDPHARY | YAPGATSISPGRMFRDL | 1920 |
| G 77 | ~ | 7.7 | |

| DADFRTQFSDVLDLYLGTHFKLDNCTMFRFPLRNAEMAKVSEISSVPASDRMVQNLLDKL | 1980 |
|--|------|
| RSDGAELLMFLNHMEKISICEIDKSTGALNVLYSVKGKITDGDRLKRKQFHASVIDSVTK | 2040 |

 $\tt KRQLKDIPVQQITYTMDTEDSEGNLTTWLICNRSGFSSMEKVSKSVISAHKNQDITLFPR$

| GGVAACITHNYKKPHRAFCFLPLSLETGLPFHVNGHFALDSARRNLWRDDNGVGVRSDWN | 2160 |
|--|------|
| | |

| NSLMTALIAPAYVELLIQLKKRYFPGSDPTLSVLQNTPIHVVKDTLKKFLSFFPVNRLDL | 2220 |
|--|------|
| | |
| QPDLYCLVKALYNCIHEDMKRLLPVVRAPNIDGSDLHSAVIITWINMSTSNKTRPFFDNL | 2280 |

| ss | |
|--|------|
| LQDELQHLKNADYNITTRKTVAENVYRLKHLLLEIGFNLVYNCDETANLYHCLIDADIPV | 2340 |
| | |

| SYVTPADIRSFLMTFSSPDTNCHIGKLPCRLQQTNLKLFHSLKLLVDYCFKDAEENEIEVVS.F | 2400 |
|--|------|
| EGLPLLITLDSVLQTFDAKRPKFLTTYHELIPSRKDLFMNTLYLKYSNILLNCKVAKVFD | 2460 |

| ISSFADLLSSVLPREYKTKSCTKWKDNFASESWLKNAWHFISESVSVKEDQEETKPTFDI | 2520 |
|--|------|
| VVDTLKDWALLPGTKFTVSANOLVVPEGDVLLPLSLMHIAVFPNAQSDKVFHALMKAGCI | 2580 |

| VVDTLKDWALLPGTKFTVSANQLVVPEGDVLLPLSLMHIAVFPNAQSDKVFHALMKAGCI I.ITSII | 2580 |
|--|------|
| QLALNKICSKDSAFVPLLSCHTANIESPTSILKALHYMVQTSTFRAEKLVENDFEALLMY | 2640 |

| FNCNLNHLMSQDDIKILKSLPCYKSISGRYVSIGKFGTCYVLTKSIPSAEVEKWTQSSSS | 2700 |
|--|------|
| S | |

| AFLEEKTHLKELYEVIGCVPVDDLEVYLKHLLPKIENLSYDAKLEHLIYLKNRLSSAEEL | 2760 |
|---|------|
| AL BERKINBERELEVICEVI VODERVIBRELER KIRKERIDI DIKKERIDI IDIKKER <u>DELEDE</u> | 2.00 |
| VLL | |
| | |

| SEIKEOLFEKLESLLIIHDANSRLKOAKHFYDRTVRVFEVMLPEKLFIPNDFFKKLEQLI | 2820 |
|--|------|
| | |
| ······································ | |

 ${\tt KPKNHVTFMTSWVEFLRNIGLKYILSQQQLLQFAKEISVRANTENWSKETLQNTVDILLH}$

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| O.G. FIG. | CLASS | | |
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| | | | |

| HIFQERMDLLSGNFLKELSLIPFLCPERAPAEFIRFHPQYQEVNGTLPLIKFNGAQVNPK | 2940 |
|--|------|
| FKQCDVLQLLWTSCPILPEKATPLSIKEQEGSDLGPQEQLEQVLNMLNVNLDPPLDKVIN | 3000 |
| NCRNICNITTLDEEMVKTRAKVLRSIYEFLSAEKREFRFQLRGVAFVMVEDGWKLLKPEE | 3060 |
| VVINLEYESDFKPYLYKLPLELGTFHQLFKHLGTEDIISTKQYVEVLSRIFKNSEGKQLDASS | 3120 |
| PNEMRTVKRVVSGLFRSLQNDSVKVRSDLENVRDLALYLPSQDGRLVKSSILVFDDAPHY | 3180 |
| KSRIQGNIGVQMLVDLSQCYLGKDHGFHTKLIMLFPQKLRPRLLSSILEEQLDEETPKVC | 3240 |
| QFGALCSLQGRLQLLLSSEQFITGLIRIMKHENDNAFLANEEKAIRLCKALREGLKVSCF | 3300 |
| EKLQTTLRVKGFNPIPHSRSETFAFLKRFGNAVILLYIQHSDSKDINFLLALAMTLKSAT | 3360 |
| DNLISDTSYLIAMLGCNDIYRIGEKLDSLGVKYDSSEPSKLELPMPGTPIPAEIHYTLLM | 3420 |
| DPMNVFYPGEYVGYLVDAEGGDIYGSYQPTYTYAIIVQEVEREDADNSSFLGKIYQIDIG | 3480 |
| YSEYKIVSSLDLYKFSRPEESSQSRDSAPSTPTSPTEFLTPGLRSIPPLFSGRESHKT-S | 3540 |
| SKHQSPKKLKVNSLPEILKEVTSVVEQAWKLPESERKKIIRRLYLKWHPDKNPFNHDIAN T.H.RA | 3600 |
| <u>EVFKHLQNEINRLEKQA</u> FLDQNADRASRRTFSTSASRFQSDKYSFQRFYT <u>SWNQEATSHK</u> | 3660 |
| SERQQQNKEKCPPSAGQTYSQRFFVPPTFKSVGNPVEARRWLRQARANFSAARNDLHKNA | 3720 |
| NEWVCFKCYLSTKLALIAADYAVRGKSDKDVKP <u>TALAQKIEEYSQQLEGLTNDVHTLEAY</u> | 3780 |
| GVDSLKTRYPDLLPFPQIPNDRFTSEVAMRVMECTACIIIKLENFMQQKV | 3830 |



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Table 1 ESTs identified by sample-sequencing of the ARSACS critical interval

| BAC clone | GenBank # | UniGene | Identity* | Tissue Source |
|---------------------|-----------------------|-------------|-----------|--|
| 235_1,_20 | AA987300 | IIs. 129092 | 221/230 | neuroendocrine lung carcinoids |
| 235_1,_20 | AA476635* | | 249/296 | total fetus |
| 235_1,_20 | AI351876* | | 272/335 | melanocyte, fetal heart, pregnant uterus (pool) |
| 235_1,_20 | W25994 | IIs. 163732 | 447/464 | retina |
| 235_1,_20 | AI377467 | IIs. 163732 | 257/263 | total fetus |
| 235_1,_20 | AA601007 | | 488/491 | schwannoma tumor |
| 235_1,_20 | AA324964 | | 214/234 | cerebellum |
| 235_1,_20, 206_1,_I | AA897178 ^b | | 238/238 | fetal lung, testis, and B-cell |
| 235_1,_20, 206_1,_I | $RI7106^{b}$ | IIs. 188560 | 747/784 | brain, adipose tissue |
| 235_I,_20, 206_I,_I | AB018273 ^b | IIs. 159492 | 4318/4318 | multiple tissue types including brain, CNS, and whole embryo |
| | | | | |

Number of homologous nucleotides between the BAC subclone sequence and the GenBank sequence. AA897178, RI7106, and AB018273 are all contained within spastin. ж. ф. *.

AA176335 and AI351876 were homologous to non-overlapping portions of the same M13 subclone sequence.

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astin ORF

Product size (bp)

| Table 2 Primers for PCR amplification of the human spa | Reverse primer |
|--|----------------|
| Table 2 Primers for P | Forward primer |
| | Primer set |

| CCTTCCAGTACTGTGTTATTTGTGAG CAAGAACTTCCTCAGGGCATC (SEQ ID NO: 22) GATGCATCTATACAACATCCGCT GGTGGGAAATAGGTTCCTTC (SEQ ID NO: 24) AAAAATGGATCCAAATGTGCT GGTGGGAAATAGGTTCTTC (SEQ ID NO: 26) GCTCCTCACTTCCTCTTGTTG GCTGAATTGGCTTCATCATGATAG (SEQ ID NO: 28) AGCAATCAGATTGAAGC GATGGGAATGTCATCATGATGG (SEQ ID NO: 30) GGGGAGAAGTTGAACACTT GATGGGAATGTCATCATGATGG (SEQ ID NO: 32) TCCAAAGCATTGAACACTTAC CAGGTCCCGTAAGACTCAG (SEQ ID NO: 34) TCCAAAGCATTGAACACTTAC CAGGTCCCGTAAGACTCAG (SEQ ID NO: 34) CAATGGGTGCTTTGCATAC CAGAACATCCGAAACTCAG (SEQ ID NO: 34) GCTGGCTGCAAACATCCTTCAA (SEQ ID NO: 36) TTCCGCGAACTTTTGAAACC ACACAACTCGGCAAAGCTCAG (SEQ ID NO: 46) GTGAATGGTCCAA ATATTCGTCGGCAAAGCTCAG (SEQ ID NO: 56) TTCCGCGAACTTGCAAACTCAGAAGCGAAGCTCAGAAGCTCAGAAGCCAAAGAAGAAGAAACAATTCCAGCAAACTCAGAAGAAGAAGAAGAAACAAAAAAAA | | | | | | | | | | | | | | | | | | | | | | EU |)H(|
|--|----------------------------|-------------------------|--------------------------|-----------------------|------------------------|------------------------|-----------------------|-----------------------|------------------------|------------------------|-----------------------|--------------------------|-----------------------|----------------------|-----------------------|-----------------------|------------------------|--------------------------|-----------------------|-----------------------|------------------------|--------------------------|---------------------------------------|
| CCTTCCAGTACTGTGTTATTTGTGAG CAAGAACTTCCTCAGGGCATC GATGCATCTATACAACATCCGCT GATGGGAAATAGGTTCCTTC AAAAATGGAAATCCCAAATGTGCT GACATCCTCCTCTTGTTG GCACTCAAGGCTTCATGATAA AGCAATCCAGCAAGC GATGGGAATTTGGTTCATCAGTGATATG GGAGAAGTTTCAGCAAACTTGG TCCAAAGCATTGAACAACTTAC GCAAAGAAGAACCACCT CAAAGAAGAAGATCCCTTCCAT GCAACAATCCGCAAACTTAC GCAACAATCCGCAAACTTAC GCAACAATCCGCAAACTTAC GCAACAATCCGCAAACTTTAGAACC GCAACAATCCGCAAACTTTAGAACC GAACAATCCGCAAACTTTTAGAACC GAACAATCCGCAAAGCTTAC GCAACAAGCCACAAATGGTCCAG TTCCGCGAACTTTTTAGAACC GAACAATCCGCAAAGCTCAT TTCCGCGAACTTTTTAGAACC GCAACAAGGCCACATTTAGAACC GAACAATCCAAAGCAAATGGTCCAG GCAACAAGGCCACTTTTAGAACC GAAAGAAGAAGAAGAAGC TGAAATGGTCCAT ACCACAAAGAAGAAGC TGAAAGAAGAAGAAACC TGAAAGAAGAAGAATCCAAAAGC TGAAAGAAGAAGAAACC TGAAAGAAGAAAACC TGAAAGAAGAAAACC TGAAAGAAAAGA | 603 | 581 | 592 | 602 | 611 | 624 | 631 | 620 | 604 | 159 | 625 | 979 | 624 | 648 | 609 | 631 | 609 | 645 | 618 | 612 | 647 | 654 | 638 |
| CCTTCCAGTACTGTGTTATTTGTGAG GATGCATCTATACAACATCGCT AAAAATGAGAATCCAAATGTGCT AGCAATCAGATTCCACAAGC GGGAGAAGTTGACAAGTTGAA TCCAAAGCATTGACAAGCT CAATGGGTGCTTTGCTGTTAC GCTGCCTCCACACACCCT CAACAACCATTCCAAAGTTGAA TCCGCGAACTTTTTGAAACC GAACAATCCGCTTCCTTCCT CAACCAAAGGCGACAATC GAACAATCCGCTTCCTTCCAT TTCCGCGAACTTTTTGAAACC GAACAAAGGCGACAAATC GCACCACACGCAAAACC CAACGCCAAAGGCCAAATC AAATGATTTTGAGCCAAAGC CATCCTGCCCTATTCTTCCAG TGACAAGCCCTATTCTTCCAG TGACAAGCCCTATTCTTCCAG TGACAAGCCCTATTCTTCCAG TGACAAGCCCTATTCTTCCAG TGACAAGCCCTATTCTTCCAG TGACAAGCCCTATTCTTCCAG TGACAAGCCCTATTCTTCCAG TGACAAGCCCTATTCTTCCAG TGACAAGCCCTAATTCCTCCAG TGACAAAGCCCTAATTCCTCCAG TGACAAGCCCTAATTCCTCCAG TGACAACCCTAATTCCTCCAG TGACAACCCTAATTCCTCCAG TGACAACCCTAATTCCTCCAG TGACAACCCTAATTCCTCCAG TGACAACCCTAATTCCTCCCTAATTCCTCCTCACATTCCTCC | (SEQ ID NO: 22) | (SEQ ID NO: 24) | (SEQ ID NO: 26) | (SEQ ID NO: 28) | (SEQ ID NO: 30) | (SEQ ID NO: 32) | (SEQ ID NO: 34) | (SEQ ID NO: 36) | (SEQ ID NO: 38) | (SEQ ID NO: 40) | (SEQ ID NO: 42) | (SEQ ID NO: 44) | (SEQ ID NO: 46) | (SEQ ID NO: 48) | (SEQ ID NO: 50) | (SEQ ID NO: 52) | (SEQ ID NO: 54) | (SEQ ID NO: 56) | (SEQ ID NO: 58) | (SEQ ID NO: 60) | (SEQ ID NO: 62) | (SEQ ID NO: 64) | (SEQ ID NO: 66) |
| NO: 21) CCTTCCAGTACTGTGTTATTTGTGAG NO: 23) GATGCATCTATACAACATCCGCT NO: 25) AAAAATGAGAATCCAAATGTGCT NO: 27) GCTCCTCACTTCCTCTTGTTG NO: 29) AGCAATCAGATTCCAGCAAGC NO: 31) GGGAGAGTTGACAAGTTGGA NO: 33) TCCAAAGCATTGACACCT NO: 33) TCCAAAGCATTTGAAACC NO: 34) GCTGGCTGCTTTCCTTCCTT NO: 35) CAATGGTGCTTTTGAAACC NO: 47) GTGAATGGCCACTTTGCAG NO: 47) GTGAATGGCCACTTTGCAG NO: 51) TGACATTTCCAGCAAACC NO: 53) AAATGATTTTGAGGCCACTTTG NO: 53) ACACTCAGCCAAAAGCAAAGC NO: 53) ACACTCAGCCAAAAGCAAAGC NO: 53) ACAGTAGACTAAAGCAAAGC NO: 53) TGACATTTTTGAGGCAAAGC NO: 53) TGACATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT | CAAGAACTTCCTCAGGGCATC | GGTGGGAAATAGGTTCCTTC | GCACTAAGGCTAGGTTTTGTGAAG | CGTGAATTGGCTTCATGATAA | GATGGGAATGTCAGTGATATGG | CTTTGGTTCATCACTGGGAAG | CAGGTCCCGTAAGACACTCAG | CGAAGAACTCCCGAGAACTCA | GCAAACATGGTTTCAGGCTTA | ATTATTCGTCGCCAAAGCTGA | ACACAAAGTGCTGGCCCTTGC | ATACAGCACATTTAGAGCTCCAGT | GCAATTCAACATATGCAGGAG | TGATATCAGCAGGGTCACAT | GCCATGCATTCTTAAGCCAAG | AGCGCCACTGATGGATTTAT | TTCCACCCAGGATGTCATAAA | ATCAAGAGGAGGATCCAGGTT | TAAAGCGCAAGGTCTCGTACA | TCTGCTGTGGGGAATAGGATT | TGCTTTGAGAGCTTTCCTCAG | GTAAGTCTGTCCGGCTGAAGG | TTCGTGCTACACACATTCAAGA |
| NO: 23) NO: 23) NO: 23) NO: 23) NO: 23) NO: 43) NO: 43) NO: 43) NO: 43) NO: 43) NO: 43) NO: 43) NO: 43) NO: 43) NO: 53) NO: 53) NO: 53) NO: 53) NO: 53) NO: 53) | CCTTCCAGTACTGTGTTATTTGTGAG | GATGCATCTATACAACATCCGCT | AAAATGAGAATCCAAATGTGCT | GCTCCTCACTTCCTCTTGTTG | AGCAATCAGATTCCAGCAAGC | GGGAGAAGTTGACAAAGTTGGA | TCCAAAGCATTGAACACACCT | CAATGGGTGCTTTGCTGTTAC | GCTGGCTGCAAACAGATACTAC | CAAACAATCCGCTTCCTTCCAT | TTCCGCGAACTTTTTGAAACC | GATGCAAAGGCGACAGAAATC | GCATCAGACAGAATGGTCCAG | GTGAATGGCCACTTTGCACT | ACCACACACAAACAGTAGCA | TGACATTTCCAGCTTTGCTGA | AAATGATTTTGAGGCACTTTTG | ACAGTAGACTAAAGCAAGCAAAGC | CATCCTGCCCTATTCTTCCAG | TGAGGCCAAACAATTAGATCC | GCAAAGCCCTAAGAGAAGGATT | TGAAAGAGAAGATGCTGACAATTC | (SEQ ID NO: 66) CATCCCGATTTCAGTCAGACA |
| | (SEQ ID NO: 21) | (SEQ ID NO: 23) | (SEQ ID NO: 25) | (SEQ ID NO: 27) | (SEQ ID NO: 29) | (SEQ ID NO: 31) | (SEQ ID NO: 33) | (SEQ ID NO: 35) | (SEQ ID NO: 37) | 0 (SEQ ID NO: 39) | 1 (SEQ ID NO: 41) | 2 (SEQ ID NO: 43) | 3 (SEQ ID NO: 45) | 4 (SEQ ID NO: 47) | 5 (SEQ ID NO: 49) | 16 (SEQ ID NO: 51) | 7 (SEQ ID NO: 53) | 8 (SEQ ID NO: 55) | 9 (SEQ ID NO: 57) | 0 (SEQ ID NO: 59) | 1 (SEQ ID NO: 61) | 22 (SEQ ID NO: 63) | 23 (SEQ ID NO: 66) |



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SUBCLASS E. O.G. CLASS ₽

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ROD
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                                        DNA
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DEFINITION
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ACCESSION
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             AF193557.1
                         GI:6907043
VERSION
KEYWORDS
SOURCE
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  ORGANISM
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REFERENCE
                (bases 1 to 11493)
             Engert, J.C., Berube, P., Mercier, J., Dore, C., Lepage, P., Ge, B.,
  AUTHORS
             Bouchard, J.P., Mathieu, J., Melancon, S.B., Schalling, M.,
             Lander, E.S., Morgan, K., Hudson, T.J. and Richter, A.
             ARSACS, a spastic ataxia common in northeastern Quebec, is caused
  TITLE
             by mutations in a new gene encoding an 11.5-kb ORF
             Nat. Genet. 24 (2), 120-125 (2000)
  JOURNAL
  MEDLINE
             20120709
REFERENCE
                (bases 1 to 11493)
             Engert, J.C., Berube, P., Dore, C., Lepage, P., Ge, B., Hudson, T.J. and
  AUTHORS
             Richter, A.
  TITLE
             Direct Submission
             Submitted (08-OCT-1999) Genome Centre, Montreal General Hospital,
  JOURNAL
             1650 Cedar Ave., Montreal, QC H3G 1A4, Canada
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                       /protein_id="AAF31263.1"
                       /db xref="GI:6907044"
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SUBCLASS O.G. FIG. CLASS

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THE TRACE! NTPVPIYHSRNPSKLVMKPIHECCYCDIKVDDLNDLLEDSVEPIILVHEDIPMKTAE WLKVPCLSTRLINPENMGFEQSGQREPLTVRIKNILEEYPSVSDIFKELLQNADDANA TECSFMIDMRRNMDIRENLLDPGMAACHGPALWSFNNSEFSDSDFLNITRLGESLKRG EVDKVGKFGLGFNSVYHITDIPIIMSREFMIMFDPNINHISKHIKDRSNPGIKINWSK OOKRLRKFPNOFKPFIDVFGCOLPLAVEAPYSYNGTLFRLSFRTQQEAKVSEVSSTCY NTADIYSLVDEFSLCGHRLIIFTQSVNSMYLKYLKIEETNPSLAQDTIIIKKKVCPSK ALNAPVLSVLKEAAKLMKTCSSSNKKLPTDVPKSSCILQITVEEFHHVFRRIADLQSP LFRGPDDDPATLFEMAKSGQSKKPSDELPQKTVDCTTWLICTCMDTGEALKFSLNESG RRLGLVPCGAVGVLLHETQEQKWTVKPHIGEVFCYLPLRIKTGLPIHINGCFAVTSNR KEIWKTDTKGRWNTTFMRHVIVKAYLQALSVLRDLAIGGELTDYTYYAVWPDPDLVHD DFSVICKGFYEDIAHGKGKELTRVFSDGSMWVSMKNVRFLDDSILQRKDVGSAAFKIF LKYLKKTGSKNLCAVELPSSVKAGFEEAGCKQILLENTFSEKQFFSEVFFPNIQEIEA ELRDPLMNFVLNEKLDEFSGILRVTPCVPCSLEGHPLVLPSRLIHPEGRVAKLFDTKD GRFPYGSTQDYLNPIILIKLVQLGMAKDDILWDDMLERAESVAEINKSDHAAACLRSS ILLSLIDEKLKIKDPRAKDFAAKYQTIPFLPFLTKPAGFSLEWKGNSFKPETMFAATD ${\tt IYTAEYQDIVCLLQPILNENSHSFRGCGSVSLAVKEFLGLLKKPTVDLVINQLKQVAK}$ SVDDGITLYQENITNACYKYLHEAVLQNEMAKATIIEKLKPFCFILVENVYVESEKVS FHLNFEAAPYLYQLPNKYKNNFRELFESVGVRQSFTVEDFALVLESIDQERGKKQITE ENFQLCRRIISEGIWSLIREKRQEFCEKNYGKILLPDTNLLLLPAKSLCYNDCPWIKV KDSTVKYCHADIPREVAVKLGAIPKRHKALERYASNICFTALGTEFGQKEKLTSRIKS ILNAYPSEKEMLKELLQNADDAKATEICFVFDPRQHPVDRIFDDKWAPLQGPALCVYN NQPFTEDDVRGIQNLGKGTKEGNPCKTGHYGIGFNSVYHITDCPSFISGNDILGIFDP HARYAPGATSVSPGRMFRDLDADFRTQFSDVLDLYLGNHFKLDNCTMFRFPLRNAEMA QVSEISSVPSSDRMVQNLLDKLRSDGAELLMFLNHMEKISICEIDKATGGLNVLYSVK GKITDGDRLKRKQFHASVIDSVTKKRQLKDIPVQQITYTMDTEDSEGNLTTWLICNRS GFSSMEKVSKSVISAHKNQDITLFPRGGVAACITHNYKKPHRAFCFLPLSLETGLPFH VNGHFALDSARRNLWRDDNGVGVRSDWNNSLMTALIAPAYVELLIQLKKRYFPGSDPT LSVLQNTPIHVVKDTLKKFLSFFPVNRLDLQPDLYCLVKALYSCIHEDMKRLLPVVRA

Figure 8B



SUBCLASS

O.G. FIG.

App No.:

Title Inventors:

09/693,205 Identification of ARSACS.

Thomas J. Hudson, et al.

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PNIDGSDLHSAVIITWINMSTSNKTRPFFDNLLQDELQHLKNADYNITTRKTVAENVY RLKHLLLEIGFNLVYNCDETANLYHCLVDADIPVSYVTPADVRSFLMTFSSPDTNCHI GKLPCRLQQTNLKLFHSLKLLVDYCFKDAEESEFEVEGLPLLITLDSVLQIFDGKRPK FLTTYHELIPSRKDLFMNTLYLKYSSVLLNCKVAKVFDISSFADLLSSVLPREYKTKN CAKWKDNFASESWLKNAWHFISESVSVTDDQEEPKPAFDVIVDILKDWALLPGTKFTV STSOLVVPEGDVLIPLSLMHIAVFPNAQSDKVFHALMKAGCIQLALNKICSKDSALVP LLSCHTANIDSPASILKAVHYMVQTSTFRTEKLMENDFEALLMYFNCNLSHLMSQDDI KILKSLPCYKSISGRYMSIAKFGTCYVLTKSIPSAEVEKWTQSSSSAFLEEKVHLKEL YEVLGCVPVDDLEVYLKHLLPKIENLSYDAKLEHLIYLKNRLASIEEPSEIKEQLFEK LESLLIIHDANNRLKQAKHFYDRTVRVFEVMLPEKLFIPKEFFKKLEQVIKPKNQAAF MTSWVEFLRNIGLKYALSQQQLLQFAKEISVRANTENWSKETLQSTVDILLHHIFQER MDLLSGNFLKELSLIPFLCPERAPAEYIRFHPQYQEVNGTLPLIKFNGAQVNPKFKQC DVLQLLWTSCPILPEKATPLSIKEQEGSDLAPQEQLEQVLNMLNVNLDPPLDKVINNC RNICNITTLDEEMVKTRAKVLRSIYEFLSAEKREFRFQLRGVAFVMVEDGWKLLKPEE VVINLEYEADFKPYLYKLPLELGTFHQLFKHLGTEDIISTKQYVEVLSRIFKSSEGKQ LDPNEMRTVKRVVSGLFKSLQNDSVKVRSDLENARDLALYLPSQDGKLVKSSILVFDD APHYKSRIQGNIGVQMLVDLSQCYLGKDHGFHTKLIMLFPQKLRPRLLSSILEEQLDE ETPKVCQFGALCSLQGRLQLLLSSEQFITGLIRIMKHENDNAFLANEEKAIRLCKALR EGLKVSCFEKLQTTLRVKGFNPIPHSRSETFAFLKRFGNAVILLYIQHSDSKDINFLL ALAMTLKSATDNLISDTSYLIAMLGCNDIYRISEKLDSLGVKYDSSEPSKLELPMPGT PIPAEIHYTLLMDPMNVFYPGEYVGYLVDAEGGDIYGSYQPTYTYAIIVQEVEREDAD NTSFLGKIYQIDIGYSEYKIVSSLDLYKFSRPDESSQNRDSAPTTPTSPTEFLTPGLR SIPPLFSGKESHKSPSTKHHSPRKLKVNALPEILKEVTSVVEQAWKLPESERKKIIRR LYLKWHPDKNPENHDIANEVFKHLQNEINRLEKQAFLDQNADRASRRTFSTSASRFQS DKYSFQRFYTSWNQEATSHKSERQQQSKEKCPPSAGQTYSQRFFVPPTFKSVGNPVEA RRWLRQARANFSAARNDLHKNANEWVCFKCYLSTKLALIAADYAVRGKSDKDVKPTAL AQKIEEYSQQLEGLTNDVHTLEAYGVDSLKTRYPDLLPFPQIPNDRFTSEVAMRVMEC TACIIIKLENFIQQKV"

Figure 8C

Inventors:

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SUBCLASS

BASE COUNT 3599 a 2281 c 2387 g 3226 t ORIGIN

1 atgaatacat tetggeetgg tegagagttg gtggtteagt ggtatecatt tagtgaagae 61 aaacgtcacc catccctttc atggcttaag atggtttgga agaatctcta tatacatttc 121 teggaagatt tgaetttatt tgatgagatg ceaettatee etagaactet aetgaatgag 181 gaccagacgt gtgtggaact catcagactc aggatcccat cagtagtcat tttagatgat 241 gaaactgaag ctcagcttcc agaattctta gcagatattg tacaaaaact tggagggatt 301 gtcctgaaaa gactagatac ctctattcag catccacttg ttaaaaaaata cattcattcc 361 ccactcccga gtgctatttt gcagataatg gagaagatac ctctacagaa gttgtgtaat 421 caaatagcat cattacttcc aacccacaaa gatgctctaa ggaagttttt ggccagctta 481 actgatacca gtgaaaaaga gaaaagaata attcaagaat tgacaatatt caaaagaatt 541 aatcactcat cagatcaagg gatttcctct tacacaaaat taaaaggatg taaagttttg 601 gatcataccg ccaagcttcc aacagatcta cggctatcag tttcagtaat agatagtagt 661 gatgaagcca ccattcgttt ggcaaacatg ttgaaaattg aaaaattgaa gactacaagc 721 tgtttaaagt ttgttttaaa agatattgga aatgcatttt atacacagga agaggtaaca 781 caacttatqc tttqqatcct tqaqaatcta tcctctctta aaaatgagaa ttcaaatgtg 841 cttgattggt taatgccact aaaattcatt catatgtccc agggacatgt ggtagcagct 901 ggtgatctct ttgatcctga tatagaagta ctaagggatc tcttttataa tgaagaagaa 961 gcttgtttcc cacctacaat ttttacctca ccagatatcc ttcactcttt gagacagatt 1021 ggcttaaaaa atgaatccag tctaaaagaa aaagatgttg tacaagtggc aagaaaaatt 1081 qaaqctttac aggtcagttc ctgtcagaat caggatgttc tcatgaagaa agccaaaaca 1141 ctcttactqq tcttqaataa aaaccagaca ctcttgcagt cttctgaagg gaagatggca 1201 ttgaagaaaa tcaaatgggt tccagcctgc aaggaaagac ctccaaatta tcccggttcc 1261 ttagtctgga aaggggatct ctgtaatctt tgtgcacctc cagatatgtg tgatgcggca 1321 catgcagttc tagtaggctc ctcacttcct cttgttgaaa gtgtccatgt gaacctggag 1381 caggogotoa goatottoac aaagootaot atcaatgotg tottaaaaca otttaaaact 1441 gttgttgact ggtatacttc aaaaaccttt agtgatgaag attactatca gttccaacat 1501 attitgcttg aaatttatgg gttcatgcat gatcatctga gtgaagggaa ggattctttt 1561 aaagcettga agtttecatg ggtttggact ggcaaaaact tttgteetet tgeecagget 1621 gtgataaagc caacccatga tctggatctt cagccttatt tatataatgt gcctaaaacc 1681 atggcaaaat tccaccagct gttcaaggct tgtggctcaa tagaagagtt gacatcagat 1741 catatttcca tggtcattca gaaagtttat ctcaaaagtg accaggagtt gagtgaagaa 1801 qaaaqtaaac aaaatcttca tctcatgttg aatattatga gatggctcta tagcaatcag 1861 attocagcaa gccctaatac accagttoot atttatcaca gcagaaatcc ttocaaactt 1921 gtcatgaagc caattcatga atgctgttat tgtgacatca aagttgatga cctcaatgac 1981 ttgcttgaag attcagtgga accaattatc ttggtacatg aagatatacc catgaaaact 2041 gcagaatggc taaaagttcc gtgccttagt acaagactga tcaatcctga aaacatgggg 2101 tttqaqcaqt caqqqcaaaq aqaqcctctt actgtaagga ttaaaaaatat tttggaagaa 2161 taccettecg tgtcagatat ttttaaagag ctacttcaaa atgctgatga tgcaaatgce 2221 acagaatgca gcttcatgat tgatatgaga aggaatatgg acatacggga aaatctcctg 2281 gacccaggga tggcagcttg tcatggacct gctctgtggt cattcaacaa ttctgaattc 2341 tcaqattcaq atttcttaaa cataacqaqq ttaqqaqaqt ctttaaaaaag gggagaagtt 2401 gacaaggttg ggaaatttgg tcttggtttt aattctgtgt accacatcac tgacattccc 2461 atcattatga gcagagaatt tatgataatg tttgatccaa acataaatca tatcagcaaa 2521 cacattaaag atagatcgaa tootggaato aaaattaatt ggagtaagca gcagaaaaga 2581 cttaggaagt tccccaacca gttcaaacca tttatagatg tatttggctg tcagttacct 2641 ttggctgttg aagctcctta cagctacaat ggaactcttt tccgactgtc ctttagaaca 2701 cagcaggaag caaaagtgag tgaagttagc agtacttgct acaatactgc ggatatttac 2761 tccctagtgg atgaatttag tctttgtggg cacagactta tcatttttac tcagagtgta 2821 aactcgatgt atttgaaata cttgaaaatt gaagaaacca atcctagctt agcacaagat 2881 acaatcataa ttaagaaaaa agtttgcccc tccaaagcat tgaatgcacc agttttaagt 2941 gttttaaaag aagctgctaa actcatgaag acttgtagca gcagcaacaa gaagcttccc 3001 acggatgtgc caaagtcatc ttgcattctt cagatcacag tcgaagaatt ccaccatgtg 3061 tttaggagga ttgctgactt acagtcacca ctatttcgag gtccagatga tgacccagct 3121 actetettg aaatggetaa atetggeeaa teaaaaaage cateagatga gttgeeacaa 3181 aagacagtag attgtaccac atggettata tgcacatgca tggatacagg agaagetete

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App No.: Title:

Inventors:

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Identification of ARSACS . . . Thomas J. Hudson, *et al*.

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APPROVED O.G. FIG.

BY CLASS SUBCLASS

DRAFTSMAN

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| | | | | | caaaaggtcg | |
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| 3541 | ctagccattg | gtggtgagct | gactgattat | acttactatg | cagtgtggcc | tgatcctgat |
| 3601 | ctagttcatg | atgacttctc | tgtgatctgt | aaaggatttt | atgaagacat | tgctcatggg |
| 3661 | aaggggaagg | agttgaccag | agtcttctct | gatgggtcta | tgtgggtttc | catgaagaat |
| 3721 | gtgaggtttc | tggatgactc | tatacttcaa | aggaaagatg | ttggttcagc | agccttcaag |
| 3781 | atatttctga | agtacctcaa | gaaaacagga | tccaaaaacc | tctgtgctgt | tgagcttcct |
| 3841 | tcttcagtaa | aagcaggatt | tgaagaggct | ggctgtaaac | agatactgct | ggaaaataca |
| 3901 | ttttcagaga | aacagttctt | ttcagaagtc | ttctttccta | atatccagga | aattgaagca |
| 3961 | gaacttagag | atcctctgat | gaattttgtc | ctaaatgaaa | aacttgatga | gttctcagga |
| 4021 | attcttcgtg | ttaccccttg | tgttccttgc | tccttggagg | gccatccttt | ggttttgcct |
| 4081 | tcaagattga | tccatcctga | aggacgagtt | gcaaagttat | ttgatactaa | agatggaaga |
| 4141 | ttcccttatg | gttccacaca | ggattacctc | aatcctatta | tcttgattaa | gctcgttcag |
| | | | | | tagagcgtgc | |
| 4261 | gctgagatta | ataaaaqtqa | ccatgctgct | gcctgcttaa | ggagtagtat | tctgctaagc |
| 4321 | cttattgatg | agaagctaaa | aataaaqqat | cctagagcaa | aggattttgc | tgcaaaatat |
| | | | | | gtttttcttt | |
| | | | | | acatttacac | |
| | | | | | attcccattc | |
| | | | | | tactaaagaa | |
| | | | | | ttgatgatgg | |
| | | | | | atgaagcagt | |
| | | | | | tttgtttcat | |
| | | | | | actttgaagc | |
| | | | | | agctttttga | |
| | | | | | tggagtctat | |
| | | | | | gccgacgaat | |
| 5041 | ggcatctgga | gtctcattag | agaaaagaga | caagaatttt | gtgagaaaaa | ttatqqcaaa |
| 5101 | atattactgc | cagacactaa | cctactacta | ctccctacta | agtcattatg | ctacaatgac |
| 5161 | tatccctaga | taaaagtaaa | ggactccact | gtcaagtatt | gccatgccga | cataccccqq |
| 5221 | gaagtagctg | taaaacttgg | tgcaatacca | aagagacata | aagcattaga | aagatatgca |
| | | | | | agaaagaaaa | |
| | | | | | aaatgctgaa | |
| | | | | | tgtttgatcc | |
| | | | | | aagggccagc | |
| | | | | | ttcagaatct | |
| 5581 | accaaagaag | ggaatcettg | caaaacagga | cattatggaa | tcggattcaa | ttccgtttat |
| 5641 | catattacag | actoccette | ttttatttct | ggcaatgaca | tcctgggtat | ttttgatccc |
| | | | | | gacgcatgtt | |
| | | | | | tgtacttggg | |
| | | | | | atgcagagat | |
| | | | | | agaatctttt | |
| 5941 | caatctaata | agacagaact | tctaatgttt | ctcaaccaca | tggagaaaat | atctatttgt |
| 6001 | gaatagata | addccacadd | aggtctgaat | gtgctctatt | cagtaaaagg | caagatcact |
| 6061 | gatacagaca | gettgeeeg | gaagcaattc | cacacctcta | taattgacag | tottactaaa |
| 6121 | aacagagacc | tcaaggacat | accadttcaa | caaataacct | acactatgga | tactgaggat |
| | | | | | caggattttc | |
| 6241 | asactateea | accegaceae | atcacctcac | aacaaccaac | atatcaccct | tttcccacat |
| 6301 | antagantag | cadcctdcat | tactcacaat | tataaaaaacc | cccacagagc | cttctacttt |
| 6361 | ctacctatat | ctttagagag | agggctgcaac | tttcatctca | atggccactt | tactctagat |
| 6421 | tragreears | gaagttgtg | acatastast | aatagagtta | gtgttcgaag | tgactggaet |
| 6401 | aatantttaa | tracarratt | aataggacgac | ccatatotto | agttactaat | ccagttaass |
| 65/1 | aacagccatett | tecetaatta | tracreases | ttatcacttt | tacagaacac | accentrest |
| | | | | | cagttaacag | |
| 6661 | caccccaact | tatattoott | antagence | ctttacactt | gcattcatga | adacatosao |
| 2001 | caycogyact | cacactyctt | ugcaaaagca | cccacaget | gcaccacga | agacacgaag |



Inventors:

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APPROVED O.G. FIG.

BY CLASS SUBCLASS

DRAFTSMAN

| | cgtcttttgc | | | | | |
|------|------------|------------|------------|------------|----------------|------------|
| | ataattactt | | | | | |
| | ctacaggatg | | | | | |
| 6901 | gtcgcagaga | atgtctacag | actgaagcac | ctgctcttag | aaattggttt | caacttggtt |
| 6961 | tataactgtg | atgaaactgc | taacctttac | cattgccttg | tagatgcaga | tatccctgtc |
| | agctatgtga | | | | | |
| 7081 | aattgccata | ttgggaagct | gccttgtcgt | cttcagcaga | ctaacctaaa | actttttcac |
| | agtttaaaac | | | | | |
| 7201 | gagggactgc | ccctactcat | tacactggac | agtgtcttgc | agatttttga | tggtaaacga |
| 7261 | cccaagtttc | taacaacata | ccatgaatta | attccatcgc | gtaaagactt | gtttatgaac |
| 7321 | accttatact | tgaaatacag | tagtgttttg | ttgaactgca | aagttgcaaa | agtgtttgac |
| 7381 | atttccagct | ttgctgactt | actctcttct | gtgttgcctc | gtgagtacaa | gaccaaaaac |
| 7441 | tgtgcaaagt | ggaaagacaa | ttttgccagt | gaatcttggc | ttaagaacgc | atggcatttt |
| 7501 | atcagtgaat | cagtaagtgt | aacggatgat | caggaagaac | caaagccagc | atttgatgtc |
| | attgttgaca | | | | | |
| | agtcagcttg | | | | | |
| 7681 | gtgttcccaa | atgctcagag | tgataaggtt | tttcacgctc | tgatgaaagc | tggctgtatt |
| | cagctggctt | | | | | |
| | cacacagcaa | | | | | |
| | acgtcaacat | | | | | |
| | ttcaactgta | | | | | |
| | ccatgctaca | | | | | |
| | gtgcttacca | | | | | |
| | gcgtttcttg | | | | | |
| | gtagatgatc | | | | | |
| | gatgcaaagt | | | | | |
| | tcagagatta | | | | | |
| | aacaatcgac | | | | | |
| | atgcttcctg | | | | | |
| | aaacctaaaa | | | | | |
| | ctgaagtacg | | | | | |
| | gcaaatacag | | | | | |
| | cacatattcc | | | | | |
| | ataccattct | | | | | |
| | caggaggtaa | | | | | |
| | ttcaagcaat | | | | | |
| | gccacaccgt | | | | | |
| | gaacaagttt | | | | | |
| | aattgcagaa | | | | | |
| | aaggtcctaa | | | | | |
| | cttcggggtg | | | | | |
| | gtagtgataa | | | | | |
| | gagcttggca | | | | | |
| | aagcaatatg | | | | | |
| | cctaatgaaa | | | | | |
| | gattcagtca | | | | | |
| | agccaggatg | | | | | |
| | aaaagtagga | | | | | |
| | ttagggaaag | | | | | |
| | cctcgtctgc | | | | | |
| | cagtttggcg | | | | | |
| | ttcatcacag | | | | | |
| | gaagaaaaag | | | | | |
| | gagaagcttc | | | | | |
| | gaaactttcg | | | | | |
| | tcagacagca | | | | | |
| | gacaatttga | | | | | |
| | _ | - | | | · - | - |



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APPROVED O.G. FIG.

BY CLASS SUBCLASS

DRAFTSMAM

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| | | | | | actcctctga | | |
|-------|------------|------------|------------|------------|------------|------------|--|
| 10201 | ctggaactcc | ccatgcctgg | cacaccaata | cccgctgaga | tccattacac | actacttatg | |
| 10261 | gatccaatga | atgttttta | tcctggggaa | tatgttggtt | accttgtgga | tgctgaaggt | |
| 10321 | ggtgatatct | atgggtcata | ccagccaaca | tacacatacg | caattattgt | gcaagaagtt | |
| 10381 | gaaagagaag | atgctgacaa | tactagtttc | ttaggaaaga | tctatcagat | cgatattggc | |
| 10441 | tacagtgaat | ataagatagt | cagctctctt | gatctgtaca | agttctcaag | gcctgatgaa | |
| 10501 | agctcccaaa | acagagacag | tgctcccacc | acaccaacaa | gccccaccga | attcctgact | |
| 10561 | cctggtctga | gaagcatccc | tcctctttc | tctggcaagg | agagccacaa | gtctccctcc | |
| 10621 | accaaacacc | attcccccag | aaagctcaag | gtgaatgctt | taccagaaat | cttaaaagaa | |
| 10681 | gtgacatcag | tggtggagca | agcttggaag | cttccagaat | cagagcggaa | aaagatcatt | |
| 10741 | agacgcttgt | atttgaagtg | gcaccctgac | aaaaatccag | aaaatcatga | tattgctaat | |
| 10801 | gaagtgttca | agcacctgca | gaatgaaatc | aacagattag | aaaaacaggc | ttttctggat | |
| 10861 | caaaatgcag | acagagette | aagaagaaca | ttttcaacct | ctgcatctcg | atttcagtca | |
| 10921 | gacaagtact | catttcaaag | attttacact | tcgtggaatc | aagaagccac | aagtcataaa | |
| 10981 | tctgaaaggc | aacagcaaag | caaagagaaa | tgccctcctt | ctgctggaca | gacatactct | |
| 11041 | caaaggttct | ttgttcctcc | caccttcaag | tcagtgggca | atccagtgga | agcccggaga | |
| 11101 | tggttaagac | aagccagagc | aaacttctca | gctgccagga | atgaccttca | caaaaatgcc | |
| 11161 | aatgaatggg | tgtgcttcaa | gtgttacctt | tccaccaagc | tggctttgat | tgcagccgac | |
| 11221 | tatgctgtca | gggggaaatc | tgataaagat | gtaaagccaa | ctgcacttgc | acaaaagata | |
| 11281 | gaggagtaca | gtcagcagct | ggaaggactg | acaaacgatg | tgcacacatt | ggaagcttat | |
| 11341 | ggtgtagaca | gcttgaaaac | aaggtaccct | gatttgcttc | cttttccgca | gattcccaat | |
| 11401 | gacaggttca | catctgaggt | tgccatgagg | gtgatggaat | gcactgcctg | tatcatcata | |
| | aaacttgaaa | | | | | | |

Figure 8G



SUBCLASS

CLASS

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App No.:

Inventors:

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LOCUS AF193556 12793 bp DNA PRI 07-FEB-2000 DEFINITION Homo sapiens sacsin (SACS) gene, complete cds. ACCESSION AF193556 VERSION AF193556.1 GI:6907041KEYWORDS . SOURCE human.

ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 12793) AUTHORS Engert, J.C., Berube, P., Mercier, J., Dore, C., Lepage, P., Ge, B., Bouchard, J.P., Mathieu, J., Melancon, S.B., Schalling, M., Lander, E.S., Morgan, K., Hudson, T.J. and Richter, A. TITLE ARSACS, a spastic ataxia common in northeastern Quebec, is caused by mutations in a new gene encoding an 11.5-kb ORF JOURNAL Nat. Genet. 24 (2), 120-125 (2000) MEDLINE 20120709

REFERENCE 2 (bases 1 to 12793) AUTHORS Engert, J.C., Berube, P., Dore, C., Lepage, P., Ge, B., Hudson, T.J. and Richter, A. TITLE Direct Submission JOURNAL Submitted (08-OCT-1999) Genome Centre, Montreal General Hospital, 1650 Cedar Ave., Montreal, QC H3G 1A4, CanadaFEATURES Location/Qualifiers source 1..12793 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="13" /map="between D13S232 and D13S292" mRNA 1..12793 /gene="SACS" /product="sacsin" gene 1..12793 /gene="SACS" CDS 77..11566 /gene="SACS" /note="molecular chaperone" /codon_start=1 /product="sacsin" /protein_id="AAF31262.1" /db_xref="GI:6907042" /translation="

MNTFWPGRELIVOWYPFDENRNHPSVSWLKMVWKNLYIHFSEDL TLFDEMPLIPRTILEEGOTCVELIRLRIPSLVILDDESEAQLPEFLADIVQKLGGFVL KKLDASIQHPLIKKYIHSPLPSAVLQIMEKMPLQKLCNQITSLLPTHKDALRKFLASL TDSSEKEKRIIQELAIFKRINHSSDQGISSYTKLKGCKVLHHTAKLPADLRLSISVID SSDEATIRLANMLKIEQLKTTSCLKLVLKDIENAFYSHEEVTQLMLWVLENLSSLKNE NPNVLEWLTPLKFIQISQEQMVSAGELFDPDIEVLKDLFCNEEGTYFPPSVFTSPDIL HSLRQIGLKNEASLKEKDVVQVAKKIEALQVGACPDQDVLLKKAKTLLLVLNKNHTLL QSSEGKMTLKKIKWVPACKERPPNYPGSLVWKGDLCNLCAPPDMCDVGHAILIGSSLP LVESIHVNLEKALGIFTKPSLSAVLKHFKIVVDWYSSKTFSDEDYYQFQHILLEIYGF MHDHLNEGKDSFRALKFPWVWTGKKFCPLAQAVIKPIHDLDLQPYLHNVPKTMAKFHQ LFKVCGSIEELTSDHISMVIQKIYLKSDQDLSEQESKQNLHLMLNIIRWLYSNQIPAS PNTPVPIHHSKNPSKLIMKPIHECCYCDIKVDDLNDLLEDSVEPIILVHEDIPMKTAE WLKVPCLSTRLINPENMGFEQSGQREPLTVRIKNILEEYPSVSDIFKELLQNADDANA TECSFLIDMRRNMDIRENLLDPGMAACHGPALWSFNNSQFSDSDFVNITRLGESLKRG EVDKVGKFGLGFNSVYHITDIPIIMSREFMIMFDPNINHISKHIKDKSNPGIKINWSK OOKRLRKFPNOFKPFIDVFGCOLPLTVEAPYSYNGTLFRLSFRTQQEAKVSEVSSTCY NTADIYSLVDEFSLCGHRLIIFTQSVKSMYLKYLKIEETNPSLAQDTVIIKKKSCSSK ALNTPVLSVLKEAAKLMKTCSSSNKKLPSDEPKSSCILQITVEEFHHVFRRIADLQSP LFRGPDDDPAALFEMAKSGQSKKPSDELSQKTVECTTWLLCTCMDTGEALKFSLSESG RRLGLVPCGAVGVQLSEIQDQKWTVKPHIGEVFCYLPLRIKTGLPVHINGCFAVTSNR KEIWKTDTKGRWNTTFMRHVIVKAYLQVLSVLRDLATSGELMDYTYYAVWPDPDLVHD DFSVICQGFYEDIAHGKGKELTKVFSDGSTWVSMKNVRFLDDSILKRRDVGSAAFKIF LKYLKKTGSKNLCAVELPSSVKLGFEEAGCKQILLENTFSEKQFFSEVFFPNIQEIEA ELRDPLMIFVLNEKVDEFSGVLRVTPCIPCSLEGHPLVLPSRLIHPEGRVAKLFDIKD GRFPYGSTQDYLNPIILIKLVQLGMAKDDILWDDMLERAVSVAEINKSDHVAACLRSS ILLSLIDEKLKIRDPRAKDFAAKYQTIRFLPFLTKPAGFSLDWKGNSFKPETMFAATD LYTAEHQDIVCLLQPILNENSHSFRGCGSVSLAVKEFLGLLKKPTVDLVINQLKEVAK SVDDGITLYQENITNACYKYLHEALMQNEITKMSIIDKLKPFSFILVENAYVDSEKVS FHLNFEAAPYLYQLPNKYKNNFRELFETVGVRQSCTVEDFALVLESIDQERGTKQITE ENFQLCRRIISEGIWSLIREKKQEFCEKNYGKILLPDTNLMLLPAKSLCYNDCPWIKV



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PROVED O.G. FIG.

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AFTSMAN

KDTTVKYCHADI PREVAVKLGAVPKRHKALERYASNVCFTTLGTEFGQKEKLTSRIKS ILNAYPSEKEMLKELLQNADDAKATEICFVFDPRQHPVDRIFDDKWAPLQGPALCVYN NOPFTEDDVRGIONLGKGTKEGNPYKTGQYGIGFNSVYHITDCPSFISGNDILCIFDP HARYAPGATSISPGRMFRDLDADFRTQFSDVLDLYLGTHFKLDNCTMFRFPLRNAEMA KVSEISSVPASDRMVQNLLDKLRSDGAELLMFLNHMEKISICEIDKSTGALNVLYSVK GKITDGDRLKRKOFHASVIDSVTKKROLKDIPVOOITYTMDTEDSEGNLTTWLICNRS GFSSMEKVSKSVISAHKNQDITLFPRGGVAACITHNYKKPHRAFCFLPLSLETGLPFH VNGHFALDSARRNLWRDDNGVGVRSDWNNSLMTALIAPAYVELLIQLKKRYFPGSDPT LSVLONTPIHVVKDTLKKFLSFFPVNRLDLQPDLYCLVKALYNCIHEDMKRLLPVVRA PNIDGSDLHSAVIITWINMSTSNKTRPFFDNLLQDELQHLKNADYNITTRKTVAENVY RLKHLLLEIGFNLVYNCDETANLYHCLIDADIPVSYVTPADIRSFLMTFSSPDTNCHI GKLPCRLOOTNLKLFHSLKLLVDYCFKDAEENEIEVEGLPLLITLDSVLQTFDAKRPK FLTTYHELIPSRKDLFMNTLYLKYSNILLNCKVAKVFDISSFADLLSSVLPREYKTKS CTKWKDNFASESWLKNAWHFISESVSVKEDQEETKPTFDIVVDTLKDWALLPGTKFTV SANQLVVPEGDVLLPLSLMHIAVFPNAQSDKVFHALMKAGCIQLALNKICSKDSAFVP LLSCHTANIESPTSILKALHYMVQTSTFRAEKLVENDFEALLMYFNCNLNHLMSQDDI KILKSLPCYKSISGRYVSIGKFGTCYVLTKSIPSAEVEKWTQSSSSAFLEEKIHLKEL YEVIGCVPVDDLEVYLKHLLPKIENLSYDAKLEHLIYLKNRLSSAEELSEIKEQLFEK LESLLIIHDANSRLKQAKHFYDRTVRVFEVMLPEKLFIPNDFFKKLEQLIKPKNHVTF MTSWVEFLRNIGLKYILSQQQLLQFAKEISVRANTENWSKETLQNTVDILLHHIFQER MDLLSGNFLKELSLIPFLCPERAPAEFIRFHPQYQEVNGTLPLIKFNGAQVNPKFKQC DVLOLLWTSCPILPEKATPLSIKEQEGSDLGPQEQLEQVLNMLNVNLDPPLDKVINNC RNICNITTLDEEMVKTRAKVLRSIYEFLSAEKREFRFQLRGVAFVMVEDGWKLLKPEE VVINLEYESDFKPYLYKLPLELGTFHQLFKHLGTEDIISTKQYVEVLSRIFKNSEGKQ $\verb|LDPNEMRTVKRVVSGLFRSLQNDSVKVRSDLENVRDLALYLPSQDGRLVKSSILVFDD|$ APHYKSRIQGNIGVQMLVDLSQCYLGKDHGFHTKLIMLFPQKLRPRLLSSILEEQLDE ETPKVCOFGALCSLOGRLOLLLSSEOFITGLIRIMKHENDNAFLANEEKAIRLCKALR EGLKVSCFEKLQTTLRVKGFNPIPHSRSETFAFLKRFGNAVILLYIQHSDSKDINFLL ALAMTLKSATDNLISDTSYLIAMLGCNDIYRIGEKLDSLGVKYDSSEPSKLELPMPGT PIPAEIHYTLLMDPMNVFYPGEYVGYLVDAEGGDIYGSYQPTYTYAIIVQEVEREDAD NSSFLGKIYOIDIGYSEYKIVSSLDLYKFSRPEESSQSRDSAPSTPTSPTEFLTPGLR SIPPLFSGRESHKTSSKHQSPKKLKVNSLPEILKEVTSVVEQAWKLPESERKKIIRRL YLKWHPDKNPENHDIANEVFKHLQNEINRLEKQAFLDQNADRASRRTFSTSASRFQSD KYSFORFYTSWNOEATSHKSEROQONKEKCPPSAGQTYSQRFFVPPTFKSVGNPVEAR RWLRQARANFSAARNDLHKNANEWVCFKCYLSTKLALIAADYAVRGKSDKDVKPTALA QKIEEYSQQLEGLTNDVHTLEAYGVDSLKTRYPDLLPFPQIPNDRFTSEVAMRVMECT ACIIIKLENFMQQKV"

BASE COUNT 4163 a 2256 c 2487 g 3887 tORIGIN atgatttaca ggaagaccat gtactcagct gcagcttcta aatccagaac gatttgcacg tcttatcaaq qaaqtaatga atacattctg gcctggcaga gaattgattg ttcaatggta tccatttgat gaaaacagaa atcacccatc tgtttcatgg cttaagatgg tttggaaaaa tctttatata catttttcag aggatttgac tttatttgat gagatgccac ttatccccag aactatacta gaggaaggtc agacatgtgt ggaactcatt agactcagga ttccatcgtt agtcatttta gacgatgaat ctgaagcaca gcttccagaa tttttagcag acattgtaca aaaacttgga gggtttgtcc ttaaaaaatt agatgcatct atacaacatc cgcttattaa aaaatatatt cattcaccat taccaagtgc tgttttgcag ataatggaga agatgccatt qcaqaaattq tqtaatcaaa taacttcgct acttccaaca cacaaagatg ccctgaggaa gttcttggct agtttaaccg atagcagtga gaaagagaaa agaattattc aagaattggc aatattcaag cgcattaacc attcttctga tcagggaatt tcctcttata caaaattgaa aggttgtaaa gtcttacacc atactgccaa actcccagca gatctgcgac tttctatttc agtaatagac agtagtgatg aagctactat tcgtctggca aacatgttga aaatagaaca gttaaagacc actagctgct taaagcttgt tttaaaagat attgaaaatg cattttattc acatgaagag gtaacacagc ttatgttatg ggtccttgag aatctatctt ctcttaaaaa

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APPROVED O.G. FIG.
BY CLASS SU

| BITE | FADE tgagaatcca acagatggta ttgtaatgaa ctccttaaga | | | | | TEC |
|-----------------|---|--------------------------|------------|------------|------------|------------|
| • | RADE MADE | aatgtgcttg | agtggttaac | accattaaaa | ttcatccaga | tatcacagga |
| | acagatggta | tcagctggtg | aactctttga | ccctgatata | gaagtactaa | aggatetett |
| | ttgtaatgaa | gaaggaacct | atttcccacc | ctcagttttt | acctcaccag | atattcttca |
| | ctccttaaga | cagattggtt | taaaaaacga | agccagtctc | aaagaaaagg | atgttgtgca |
| | | aaaattgaag | | | | |
| | | aaaaccctct | | | | |
| | | atgacattga | | | | |
| တ္တ | | ggctctttgg | | | | |
| Š | | gtaggccatg | | | | |
| SUBCLASS | | ctggaaaaag | | | | |
| رم ا | | aaaattgttg | | | | |
| 22 | | cagcatattt | | | | |
| CLASS | | tcttttagag | | | | |
| | | caggctgtga | | | | |
| AAN | taatgtacct | aaaaccatgg | caaaattcca | ccaactattt | aaggtctgtg | gttcaataga |
| BY FTS | ggagttgaca | tcagatcata | tttccatggt | tattcagaag | atatatctca | aaagtgacca |
| BY DRAFTSMAN | agatctcagt | gaacaagaaa | gcaaacaaaa | tcttcatctt | atgttgaata | ttatcagatg |
| | | aatcagattc | | | | |
| | aaatccttct | aaacttatca | tgaagccaat | tcacgaatgc | tgttattgtg | acattaaagt |
| | tgatgacctt | aatgacttac | ttgaagattc | tgtggaacca | atcattttgg | tgcatgagga |
| | catacccatg | aaaactgcag | aatggctaaa | agttccatgc | cttagtacaa | gactgataaa |
| | | atgggatttg | | | | |
| | | gaagaatacc | | | | |
| | | aatgcaacag | | | | |
| | | ctcctagacc | | | | |
| | | caattctcag | | | | |
| | | gaagttgaca | | | | |
| | | attcccatca | | | | |
| | | agtaaacaca | | | | |
| | | aaaagactta | | | | |
| | | ttacctttga | | | | |
| | | agaactcaac | | | | |
| | | atttattctc | | | | |
| | | agtgtaaagt | | | | |
| | | caagatacag | | | | |
| | cacacctgtc | ttaagtgttt | taaaagaggc | tgctaagete | atgaagactt | tananataan |
| | | cttcccagtg | | | | |
| | = | catgtgttca | | | | |
| | | ccagctgctc | | | | |
| | | tcacagaaaa gctctgaagt | | | | |
| | | | | | | |
| | | gtaggagttc gaggtgtttt | | | | |
| | | tgctttgctg | | | | |
| | | aataccacgt | | | | |
| | | cgggacctgg | | | | |
| | | cctgatttag | | | | |
| | | catggaaaag | | | | |
| | | aagaacgtaa | | | | |
| | | ttcaagatat | | | | |
| | | cttccttctt | | | | |
| | | aacacatttt | | | | |
| | | gaagcagaac | | | | |
| | | tcgggagttc | | | | |
| | | - | | | | |

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| tcctttggtt | ttgccatcaa | gattgatcca | ccccgaagga | cgagttgcaa | agttatttga | | |
|------------|------------|------------|------------|------------|------------|--|--|
| tattaaagat | gggagattcc | cttatggttc | tactcaggat | tatctcaatc | ctattattt | | |
| | gttcagttag | | | | | | |
| | tcagtagctg | | | | | | |
| | ttgagtctta | | | | | | |
| | aaatatcaaa | | | | | | |
| | tggaaaggca | | | | | | |
| | gaacatcaag | | | | | | |
| | agaggttgtg | | | | | | |
| | acagttgatc | | | | | | |
| | acactgtacc | | | | | | |
| | caaaatgaaa | | | | | | |
| | gttgagaatg | | | | | | |
| tgaggcggca | ccataccttt | atcagttgcc | taataagtat | aaaaataatt | tccgcgaact | | |
| | gtgggtgtga | | | | | | |
| | caagaaagag | | | | | | |
| | agtgaaggaa | | | | | | |
| gaaaaattat | ggcaagatat | tattgccaga | tactaatctt | atgcttctcc | ctgctaaatc | | |
| | aatgattgcc | | | | | | |
| | cccagggaag | | | | | | |
| cttagaaaga | tatgcatcca | atgtctgttt | tacaacactt | ggcacagaat | ttgggcagaa | | |
| agaaaaattg | accagcagaa | ttaagagcat | ccttaatgca | tatccttctg | aaaaggaaat | | |
| | cttcttcaaa | | | | | | |
| tgatcctaga | cagcatccag | ttgatagaat | atttgatgat | aagtgggccc | cattgcaagg | | |
| | tgtgtgtaca | | | | | | |
| gaatcttgga | aaaggcacga | aagagggaaa | tccttataaa | actggacagt | atggaatagg | | |
| attcaattct | gtgtatcata | tcacagactg | cccatcttt | atttctggca | atgacatcct | | |
| gtgtatttt | gatcctcatg | ccagatatgc | accaggggcc | acatccatta | gtcccggacg | | |
| catgtttaga | gatttggatg | cagattttag | gacacagttc | tcagatgttc | tggatcttta | | |
| | cattttaaac | | | | | | |
| | aaagtttcgg | | | | | | |
| | aaactgcgct | | | | | | |
| | atttgtgaaa | | | | | | |
| | atcacagatg | | | | | | |
| | actaaaaaga | | | | | | |
| | gaggactctg | | | | | | |
| | atggagaaag | | | | | | |
| | ccacgtggtg | | | | | | |
| | tgttttttgc | | | | | | |
| | ctggattcag | | | | | | |
| | tggaataaca | | | | | | |
| | ttaaaaaaac | | | | | | |
| | attcatgttg | | | | | | |
| _ | gatctacagc | | | | | | |
| | atgaaacgtc | | | | | | |
| | gcagttataa | | | | | | |
| | aatttactac | | | | | | |
| | aaaacagtag | | | | | | |
| | ttggtttata | | | | | | |
| | cctgttagtt | | | | | | |
| | gacactaatt | | | | | | |
| | tttcatagtt | | | | | | |
| | gaagttgagg | | | | | | |
| ttttgatgca | aaacgaccca | agtttctaac | aacatatcat | gaattgattc | catcccgcaa | | |



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|-----------|----------|-----------|
| -1G. | SUBCLASS | |
| O.G. FIG. | CLASS | |
| APPROVED | λa | DRAFTSMAN |

| | | tatatttgaa | | | |
|------------|------------|------------|------------|------------|------------|
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App No.: Title

Inventors:

09/693,205

Identification of ARSACS . . Thomas J. Hudson, et al.

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